

Amendments to the Specification

Please replace the paragraph spanning page 5, line 25, to page 6, line 1, with the following replacement paragraph.

FIG. 3 represents (a) Distribution of CpG dinucleotides (vertical lines) in the 5' region of the SPARC gene showing a CpG-rich sequence (CpG island) spanning from exon 1 to intron 1; (b) Methylation-specific PCR (MSP) analysis of SPARC in pancreatic *cancer* cell lines and a non-neoplastic HPDE; the PCR products in the lanes U and M indicate the presence of unmethylated and methylated templates, respectively; (c) SPARC mRNA expression by RT-PCR in pancreatic *cancer* cell lines harboring aberrant SPARC methylation before (-) and after (+) treatment with 5-aza-2'-deoxycytidine (5Aza-dC); (d) MSP analysis of SPARC in pancreatic *cancer* xenografts; (e) MSP analysis of SPARC in normal pancreatic ductal epithelia selectively microdissected. (f) MSP analysis of SPARC in the identified cell lines.

Please replace the paragraph at page 5, lines 8-17, with the following replacement paragraph:

FIG. 5 represents (a) Semiquantitative RT-PCR analysis of SPARC expression in primary fibroblasts derived from chronic pancreatitis tissue (panc-f1), from non-cancerous pancreatic tissue from a patient with pancreatic *cancer* (panc-f3), and from pancreatic adenocarcinoma tissue (panc-f5); the bar graph shown represents relative SPARC mRNA expression for each sample normalized to the corresponding GAPDH expression; (b) Change in SPARC mRNA expression in fibroblasts (panc-f3) upon co-culture with pancreatic *cancer* cells (CFPAC1); the bar graph represents the mean.+-.SD of relative SPARC expression levels (normalized to GAPDH) from two independent PCR reactions; (c) Effect of TGF- β on SPARC mRNA expression in fibroblasts (panc-f3); the bar graph represents the mean.+-.SD of relative SPARC expression levels (normalized to GAPDH) from two independent PCR reactions.